

CACGCGTCCGCCCACGCGTCCGGTGAGACAGAGGCAAAACAAAGGTGCTGAAAGCCAGAC  
1 -----+-----+-----+-----+-----+-----+ 60  
GTGCGCAGGCGGGTGCGCAGGCCACTCTGTCTCCGTTTGTTCACGACTTTCGGTCTG  
a H A S A H A S G E T E A K Q R C \* K P D -  
ATGGAGTCAGAGATGAGTGATCCTCAGCCATTGCAGGAGGAAAGATATGATATGTCAGGT  
61 -----+-----+-----+-----+-----+-----+ 120  
TACCTCAGTCTCTACTCACTAGGAGTCGGTAACGTCCTCCTTTCTATACTATACAGTCCA  
a M E S E M S D P Q P L Q E E R Y D M S G -  
GCCCCGCTGGCCCTGACGCTGTGTGTACCAAAGCCCGGGAGGGTCCGAGGTAgACATG  
121 -----+-----+-----+-----+-----+-----+ 180  
CGGGCGGACCGGGACTGCGACACACAGTGGTTTCGGGCCCTCCCAAGGCTCCATcTGATAC  
a A R L A L T L C V T K A R E G S E V D M -  
GAGGCCCTGGAACGCATGTTCCGTTACCTGAAATTTGAAAGCACCATGAAGAGGGATCCC  
181 -----+-----+-----+-----+-----+-----+ 240  
CTCCGGGACCTTGCGTACAAGGCAATGGACTTTAACTTTCTGGTACTTCTCCCTAGGG  
a E A L E R M F R Y L K F E S T M K R D P -  
ACCGCCCAGCAATTTCTGGAAGAGTTGGATGAATTTGAGCAGACCATAGATAATTGGGAA  
241 -----+-----+-----+-----+-----+-----+ 300  
TGCGGGGTCGTTAAAGACCTTCTCAACCTACTTAAAGTCGTCTGGTATCTATTAACCCTT  
a T A Q Q F L E E L D E F Q Q T I D N W E -  
GAGCCTGTCAGCTGTGCCTTTGTGGTACTCATGGCACATGGTGAGGAAGGCCTCCTCAAG  
301 -----+-----+-----+-----+-----+-----+ 360  
CTCGGACAGTCGACACGGAACACCATGAGTACCGTGTACCACTCCTTCCGGAGGAGTTC  
a E P V S C A F V V L M A H G E E G L L K -  
GGAGAAGATGAGAAGATGGTCAGACTAGAAGACCTTTTTGAAGTCTTGAACAACAAGAAC  
361 -----+-----+-----+-----+-----+-----+ 420  
CCTCTTCTACTCTTCTACCAGTCTGATCTTCTGGAAAACTTCAGAACTTGTTGTTCTTG  
a G E D E K M V R L E D L F E V L N N K N -  
TGCAAGGCCCTGAGAGGCAAGCCAAAGGTGTACATCATCCAGGCTTGTAGAGGAGAGCAC  
421 -----+-----+-----+-----+-----+-----+ 480  
ACGTTCCGGGACTCTCCGTTTCGGTTTCCACATGTAGTAGGTCCGAACATCTCCTCTCGTG

Fig. 1A

BEST AVAILABLE COPY

```

a   C K A L R G K P K V Y I I Q A C R G E H   -
    AGAGACCCCGGTGAGGAACTACGTGGAAATGAGGAACTAGGTGGAGATGAGGAACTNGGT
481 -----+-----+-----+-----+-----+-----+ 540
    TCTCTGGGGCCACTCCTTGATGCACCTTTACTCCTTGATCCACCTCTACTCCTTGANCCA

a   R D P G E E L R G N E E L G G D E E L G   -
    GGAGATGAGGTTGCTGTGCTCAAGAACAACCCCCAAAGTATCCCAACCTATACGGATACC
541 -----+-----+-----+-----+-----+-----+ 600
    CCTCTACTCCAACGACACGAGTTCTTGTTGGGGGTTTCATAGGGTTGGATATGCCTATGG

a   G D E V A V L K N N P Q S I P T Y T D T   -
    CTCCACATCTACTCCACGGTAGAGGGGTACCTCTCCTATAGACATGACGAGAAAGGCTCT
601 -----+-----+-----+-----+-----+-----+ 660
    GAGGTGTAGATGAGGTGCCATCTCCCCATGGAGAGGATATCTGTACTGCTCTTCCGAGA

a   L H I Y S T V E G Y L S Y R H D E K G S   -
    GGCTTCATCCAGACCCTGACGGATGTGTTTCATTCATAAAAAAGGATCCATCTTAGAACTG
661 -----+-----+-----+-----+-----+-----+ 720
    CCGAAGTAGGTCTGGGACTGCCTACACAAGTAAGTATTTTTTCTAGGTAGAATCTTGAC

a   G F I Q T L T D V F I H K K G S I L E L   -
    ACAGAAGAGATCACCCGACTTATGGCAAACACGGAGGTGATGCAGGAAGGAAAACCAAGG
721 -----+-----+-----+-----+-----+-----+ 780
    TGTCTTCTCTAGTGGGCTGAATACCGTTTGTGCCTCCACTACGTCCTTCCTTTTGGTTCC

a   T E E I T R L M A N T E V M Q E G K P R   -
    AAAGTGAACCCTGAAGTCCAAAGCACCCCTCCGGAAGAAGCTCTATTTGCAATAAAAGAGA
781 -----+-----+-----+-----+-----+-----+ 840
    TTTCACTTGGGACTTCAGGTTTCGTGGGAGGCCTTCTTCGAGATAAACGTTATTTTCTCT

a   K V N P E V Q S T L R K K L Y L Q * K R   -
    GGGCAGGGAT
841 -----+ 850
    CCCGTCCCTA

a   G Q G   -
    
```

BEST AVAILABLE COPY

Fig. 1B

casp-11	-----	
casp-12	-----MAARRTHERDPIYKIKGLAKMLDGV	26
casp-1	-----MADKILRAKRQFINSVSIGTINGL	25
casp-3	-----	
casp-7	-----	
casp-6	-----	
casp-8	MDFQSCLDIAEELGSEDLAALKFLCLDYIPHKLETIEDAQKFLRLREKMLEEGNLSFLKELLFHISRWDLLVNFLLCNREEMVRELDRPQCPRLF	100
casp-2	-----MAAPSGRSQSSLHRKGLMAARRSRILAVCGMHPDHQETLKKNRVVLAKQLL	52
casp-14	-----	
casp-11	-----MAENKHPDKPLKVLQELGKEVL..TEYLEKLVQSNVLKLEEDKQKFNNNAERSDKRWVFW.DAMKKKHSKVGEMLLQTTFFSVDPG	82
casp-12	FDOLVEKNVLNGDELLKIGESASFILNKAENLVENFLEKTDMAKIFAGHIANSQEQLSLQFSNDEDDGPQKICTPSSPSESKRKVEDDEMEVNAGLAHE	126
casp-1	LDELLEKRVLNQEEMDKIKLANITAMDKARDLCDHVSKKGPQASQIFITYICNEDCYLAGILELQSAPSAETFVATEDSKGGHPSSSETKEEQN..KEDG	123
casp-3	-----MENNKTSV	8
casp-7	-----MTDDQCAAELEKVDSSSEDGVDAPDRSSI	31
casp-6	-----	
casp-8	PYRSCSFRLSEEVSELELRSFKLLNNEIPKCKLEDDLSLLEIFVEMEKRTMLAENNELTKSICDQVNSLLGKIEDYERSSTERRMSLEGREELPPSV	200
casp-2	LSLELHLLLEKDIITLEMRELTAQKGSFSQNVELLNLLPKRGPQAFDAFCEALRETROGHLEDLLTTLSDIQHVLPLSCDYDTSLPFSVCSCPPHK	152
casp-14	-----	
casp-11	SHHGLEANLEMEPEESLNTLKLCSPEEFTRLCREKTQEIYPIKEAN.GRTRKALIIICNTEFKHLSRYGANFDIIGMKGLLEDLGYDVVKEELTAEGME	181
casp-12	SHMLTAPHGLQSSEVDTLKLCPRDQFCKIKTERAKEIYPVMEKE.GRTRLALIIICNKKFDYLFDRDNADTDILNQELLENLGYSVVLKENLTAQEME	225
casp-1	TFPGLTG.....TLKFCPLEKAQKLWKENPSEIYPIIMNTT..TRTRLALIIICNTEFQHLSPRVGAQVDLREMKLLLEDLGYTVKVENLTALEMV	211
casp-3	DSKSNINNFVKTIHGSKSVDSGIYLDSSYKMDYPEMIGICIIINNKNFHS.....TGMSSRSGTDVDAANLRETFMGLKYCVRNKNDLTREDIL	97
casp-7	ISSILLKKRNASAGPVRTGRDRVPTYLYRMDQKMGKCIINNKNFKA.....TGMVVRNGTDKAGALFKCFQNLGFEVTVHNDSCAKMQ	120
casp-6	-----MTETDGFYKSREVFDAEQYKMDHKRRGVALIFNHERFFWH.....LTLPERRGTNADRNLTTRFSDLGFEVKCFNDLRAEELL	80
casp-8	LDEMSLKMAELCDSPREQDSERTSDKVYQMKNKPRGYCLIIINNDFSKA....REDITQLRKMKDRKGTDCDEALSKTFELHFEIVSYDDCTANEIH	296
casp-2	QLRLSTDATEHSLDNGDGPCLLVKPCTPEFYQAHYQLAYRLQSQPRGLALVLSNVHFTGEKDLFRSGGDVDHTLVTFLKLGYNVHVLHDQTAQEMQ	252
casp-14	-----MESEMSDPQPLQEERYDMSGARLALTLCVTK...AREGSEVDMEALERMFRYLKFESTMKROPTAQQFL	66
casp-11	SEMDKFAAL..SEHQTSDSTFLVLMHSHGLHIGCGTMHSEKTPDVLQYDTIYQIFNNCHCPGLRDKPKVIIQACRGGNSGEMWIRESSKQPLCRGVDP	279
casp-12	TELMQFAGR..PEHQSSDSTFLVFMHSHGILEGICGVKHRNKKPDVLDHDTIFKIFNNSNCRSLRNKPKILIMQACRGRYNGTIWV..STNKGIAATADTDEE	322
casp-1	KEVKEFAAC..PEHKTSDSTFLVFMHSHGIEGICGTTYSNEVSDILKVDTIFQMMNTLKCPSLKDKPKVIIQACRGEKQGVVLLKDS....VRDSEED	304
casp-3	ELMDSVK...EDHSKRSSFVFCVILSHGDEGVYGTNGP.....VELKKLSFFRGDYCRSLTGKPKLFIQACRGTELDGI.....ETDS...G	177
casp-7	DLRKASE...EDHSNSACFACVLLSHGEEDLYGKDG...TPIKDLTAHFRGDRCKTLLEKPKLFIQACRGTELDGI.....QADS...G	200
casp-6	LKTHEVST...SSHIDADCFCVFLSHGEGNHVYAYDAK....IEIQTLTGLFKGDKQSLVGKPKIFIQACRGSQHDVPVPLDMVDHQTOK...LD	169
casp-8	EILEGYQS...ADHKNKDCFICCLSHGDKGVVYGTGK...EASIDLTSYFTGSKCPSLGGKPKIFIQACRGSNFQKGVPEAGFEQNH...LE	356
casp-2	EKLQNAFQ.LPAHRVTDVCV.VALLSHGVEGGIYGVGK...LLQLQEVFLFDNANCPSLQNKPKMFIQACRGDETDRGVDDQDGKNTQSPGCEE	345
casp-14	EELDEFQQTIDNWEPEVSCAFVVLMAHGEELGKGEDEK....MVRLEDLFEVLNNKNCKALRGKPKVYIIQACRGEHROPGEELRGNEELGGDEELGG	161

BEST AVAILABLE COPY

Fig. 2A-1

casp-11 RNMEA...DAVKLSHVEKDFIAFYSTTPHLSYRDKTGGSYFITRLISCFRKHACSCHLFDIFLKVQSFEEKASHSQMPTIDRATLTRYFYLFPGN-- 373  
 casp-12 RVLSCKN.NNSITKAHVETDFIAFKSSTPHNISWRVGKTGSLFISKLDICFKKYCWYHLEEIFRKVQHSFEVPGELTQMPTIERVSMTRYFYLFPGN-- 419  
 casp-1 FLTDAIFEDDGIKKAHIEKDFIAFCSTPDNVSWRHPVRGSLFIESLIKHMKEYAWSCDLEDIFRKVRFSFEQPEFRLQMPTADRVTLTRFYLFPGH-- 402  
 casp-3 ..TDEEMAC...QKIPVEADFLYAYSTAPGYYSWRNPKGSGWFIQSLCSMLKLY..AHKLEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLT 270  
 casp-7 ..PINDIDANPRNKIPVEADFLYAYSTVPGYYSWRNPGKGSWFVQALCSILNEH..GKDLEIMQILTRVNDVRARHFESQSDPRFNEKKQIPCIVSMLT 296  
 casp-6 ..NVTQVDAASYTLPAGADFLMCYSVAEGYYSHRETVNGSWYIQDLCEMLARY..GSSLEFTELLTLVNRKVSQRRVDFCKDPAIGKKQVPCFASMLT 265  
 casp-8 ..VDS...SSHKNYIPDEADFLMGATVLMCVSYRDPVNGTWYIQSLCQSLRERC.PQGDDILSILTGVDYVSN.....KDDRRNKGKQMPQPTFTLR 474  
 casp-2 ..SDAGKEELMKMRLPTRSDMICGYACLKGNAAMRNTKRGSWYIEALTQVFSERA.C.DMHVADMLVKVNALIKER.EGYAPGTEFHRCKEMSEYCS TLC 440  
 casp-14 ..DEAVLKNNPQSIPTYTDTLHIYSTVEGYLSYRHDEKSGFIQTLTDVFIHKK.G.S..ILELTEEITRLMANT.EVMQEGKP...RKVNPEVQSTLR 251

casp-11 -----  
 casp-12 -----  
 casp-1 -----  
 casp-3 KELYFYH----- 277  
 casp-7 KELYFSR----- 303  
 casp-6 KKLHFCPKPSK- 276  
 casp-8 KKL----- 477  
 casp-2 QQLYLFPGYPPT 452  
 casp-14 KKLYLQ----- 257

Fig. 2A-2

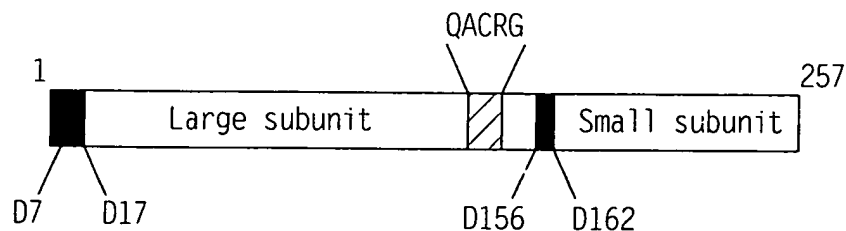
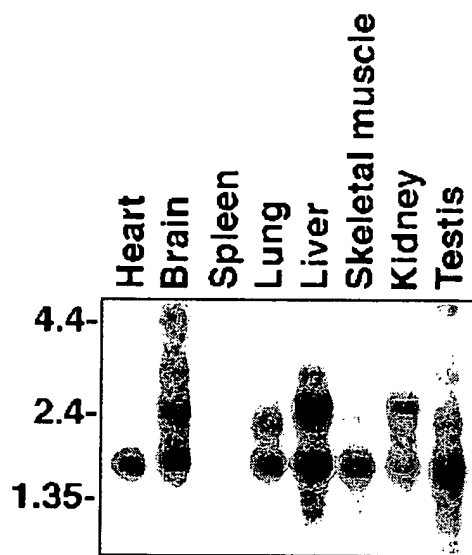


Fig. 2B

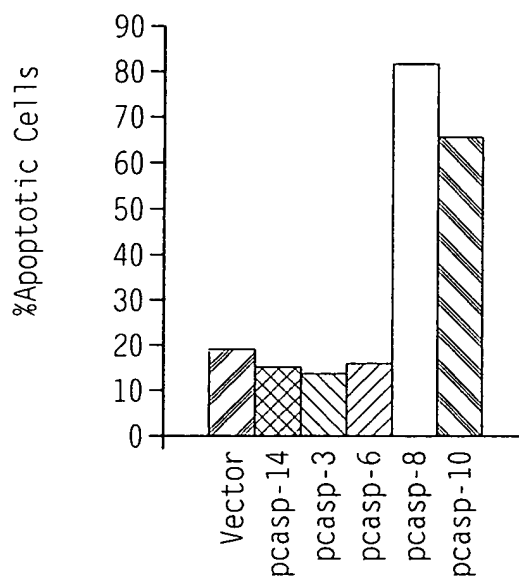
BEST AVAILABLE COPY



*Fig. 3*

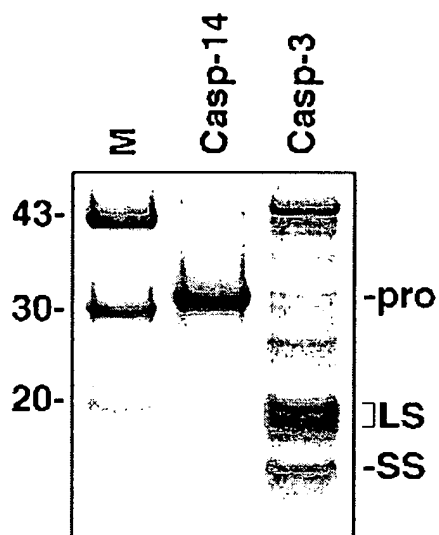
BEST AVAILABLE COPY

09989903, 112001

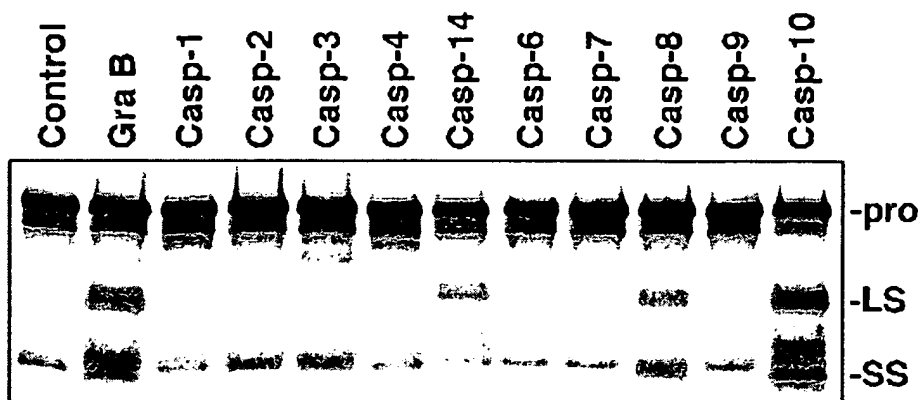


*Fig. 4*

BEST AVAILABLE COPY



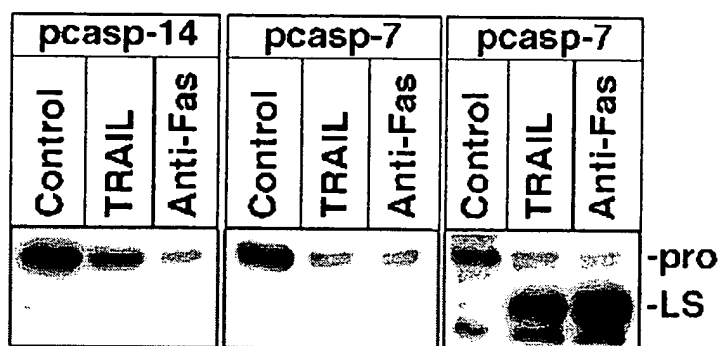
*Fig. 5A*



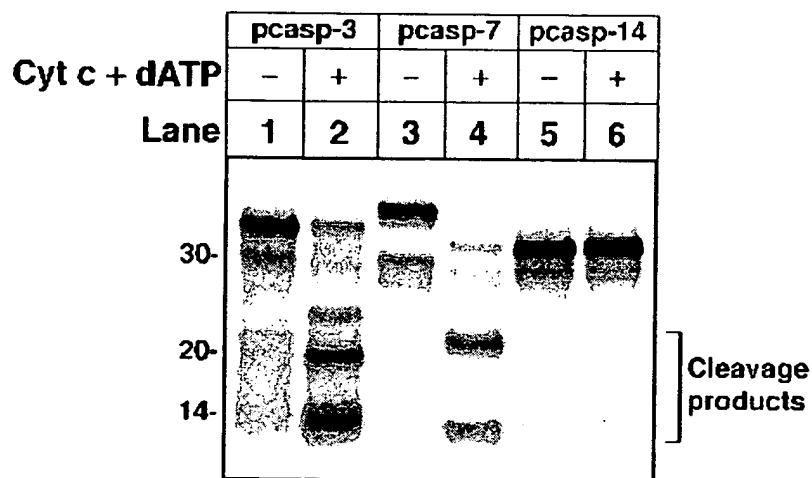
*Fig. 5B*

FIG. 5A

BEST AVAILABLE COPY



*Fig. 5C*



*Fig. 6*

BEST AVAILABLE COPY



aggatcagac aagggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57  
 Met Ser Asn

1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105  
 Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu  
 5 10 15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac 153  
 Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp  
 20 25 30 35

ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc 201  
 Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr  
 40 45 50

atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa 249  
 Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys  
 55 60 65

ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc 297  
 Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe  
 70 75 80

gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat 345  
 Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp  
 85 90 95

ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag 393  
 Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys  
 100 105 110 115

aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc 441  
 Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala  
 120 125 130

tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag 489  
 Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu  
 135 140 145

att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca 537  
 Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr  
 150 155 160

BEST AVAILABLE COPY

Fig. 7A

gat gcc ttg cac gtt tat tcc acg gta gag gga tac atc gcc tac cga 585  
 Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile Ala Tyr Arg  
 165 170 175

cat gat cag aaa ggc tca tgc ttt atc cag acc ctg gtg gat gtg ttc 633  
 His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val Asp Val Phe  
 180 185 190 195

acg aag agg aaa gga cat atc ttg gaa ctt ctg aca gag gtg acc cgg 681  
 Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu Val Thr Arg  
 200 205 210

cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa gca agg aaa acg 729  
 Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala Arg Lys Thr  
 215 220 225

aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg tat ctg cag tag 777  
 Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr Leu Gln  
 230 235 240

*Fig. 7B*

BEST AVAILABLE COPY

aggatcagac aaggggtgctg agagccggga ctcacaacca aaggagaa atg agc aat	57
Met Ser Asn	
1	
ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg	105
Pro Arg Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu	
5 10 15	
gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gac	153
Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Asp	
20 25 30 35	
ctg gat gct ctg gaa cac atg ttt cgg cag ctg aga ttc gaa agc acc	201
Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe Glu Ser Thr	
40 45 50	
atg aaa aga gac ccc act gcc gag caa ttc cag gaa gag ctg gaa aaa	249
Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu Leu Glu Lys	
55 60 65	
ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc agt tgt gcc ttc	297
Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser Cys Ala Phe	
70 75 80	
gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc aag gga gaa gat	345
Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys Gly Glu Asp	
85 90 95	
ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc ctg aac aac aag	393
Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu Asn Asn Lys	
100 105 110 115	
aac tgc cag gcc ctg cga gct aag ccc aag gtg tac atc ata cag gcc	441
Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile Ile Gln Ala	
120 125 130	
tgt cga gga gaa caa agg gac ccc ggt gaa aca gta ggt gga gat gag	489
Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly Gly Asp Glu	
135 140 145	
att gtg atg gtc atc aaa gac agc cca caa acc atc cca aca tac aca	537
Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro Thr Tyr Thr	
150 155 160	

BEST AVAILABLE COPY

Fig. 8A

gat gcc ttg cac gtt tat tcc acg gta gag gga ccc acg ccc ttc cag	585
Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Pro Thr Pro Phe Gln	
165 170 175	
gat ccc ctc tac cta ccc tct gaa gct ccc ccg aac cca cct ctc tgg	633
Asp Pro Leu Tyr Leu Pro Ser Glu Ala Pro Pro Asn Pro Pro Leu Trp	
180 185 190 195	
aat tcc cag gat aca tcg cct acc gac atg atc aga aag gct cat gct	681
Asn Ser Gln Asp Thr Ser Pro Thr Asp Met Ile Arg Lys Ala His Ala	
200 205 210	
tta tcc aga ccc tgg tgg atg tgt tca cga aga gga aag gac ata tct	729
Leu Ser Arg Pro Trp Trp Met Cys Ser Arg Arg Gly Lys Asp Ile Ser	
215 220 225	
tgg aac ttc tgacagaggt gacccggcgg atggcagaag cagagctggt	778
Trp Asn Phe	
230	
tcaagaagga aaagcaagga aaacgaaccc tgaaatccaa agcaccctcc ggaaacggct	838
gtatctgcag tag	851

*Fig. 8B*

BEST AVAILABLE COPY

aggatcagac aaggggtgctg agagccggga ctcacaacca aaggagaa atg agc aat 57  
 Met Ser Asn  
 1

ccg cgg tct ttg gaa gag gag aaa tat gat atg tca ggt gcc cgc ctg 105  
 Pro Arg Ser Leu Glu Glu Lys Tyr Asp Met Ser Gly Ala Arg Leu  
 5 10 15

gcc cta ata ctg tgt gtc acc aaa gcc cgg gaa ggt tcc gaa gaa gaa 153  
 Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser Glu Glu Glu  
 20 25 30 35

gag ctg gaa aaa ttc cag cag gcc atc gat tcc cgg gaa gat ccc gtc 201  
 Glu Leu Glu Lys Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val  
 40 45 50

agt tgt gcc ttc gtg gta ctc atg gct cac ggg agg gaa ggc ttc ctc 249  
 Ser Cys Ala Phe Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu  
 55 60 65

aag gga gaa gat ggg gag atg gtc aag ctg gag aat ctc ttc gag gcc 297  
 Lys Gly Asp Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala  
 70 75 80

ctg aac aac aag aac tgc cag gcc ctg cga gct aag ccc aag gtg tac 345  
 Leu Asn Asn Lys Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr  
 85 90 95

atc ata cag gcc tgt cga gga gaa caa agg gac ccc ggt gaa aca gta 393  
 Ile Ile Gln Ala Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val  
 100 105 110 115

ggt gga gat gag att gtg atg gtc atc aaa gac agc cca caa acc atc 441  
 Gly Gly Asp Glu Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile  
 120 125 130

cca aca tac aca gat gcc ttg cac gtt tat tcc acg gta gag gga tac 489  
 Pro Thr Tyr Thr Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr  
 135 140 145

atc gcc tac cga cat gat cag aaa ggc tca tgc ttt atc cag acc ctg 537  
 Ile Ala Tyr Arg His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu  
 150 155 160

Fig. 9A

BEST AVAILABLE COPY

gtg gat gtg ttc acg aag agg aaa gga cat atc ttg gaa ctt ctg aca 585  
 Val Asp Val Phe Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr  
 165 170 175

gag gtg acc cgg cgg atg gca gaa gca gag ctg gtt caa gaa gga aaa 633  
 Glu Val Thr Arg Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys  
 180 185 190 195

gca agg aaa acg aac cct gaa atc caa agc acc ctc cgg aaa cgg ctg 681  
 Ala Arg Lys Thr Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu  
 200 205 210

tat ctg cag tag 693  
 Tyr Leu Gln

*Fig. 9B*

BEST AVAILABLE COPY

1 MESEMSDPQLQEERYMSGARLALTLCVTKAREGSEVDMEALERMFRYL 50  
 |||. ||:||||| ||| ||: ||| |  
 1 ...MSNPRSLEEKYMSGARLALILCVTKAREGSEEDLDALAHMFRQL 46  
 51 KFESTMKRDPTAQFLEELDEFQQTIDNWEVPVSCAFVVLMAHGEEGLLK 100  
 :|||||: |||: ||| ||: ||| ||| ||  
 47 RFESTMKRDPTAEQFQEELEKFQQAIDSREDPVSCAFVVLMAHGREGFLK 96  
 101 GEDEKMRLEDLFEVLNNKNCKALRGKPKVYIIQACRGEHRDPGEELRGN 150  
 ||| ||: ||| ||| ||| ||| ||| |||  
 97 GEDGEMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQRDPG..... 140  
 151 EELGGDEELGGDEAVLKNPQSIPTYTOTLHIYSTVEGYLSYRHDEKGS 200  
 |. ||| | ||: ||: ||| ||: ||| ||: ||| |||  
 141 ETVGGDE.....IVMVIKSPQTIPTYTDALHVYSTVEGYIAYRHDQKGS 185  
 201 GFIQTLTDVFIHKKGSILELTEEITRLMANTEVMQEGKPRKVNPEVQSTL 250  
 |||| ||| :|| ||| |:|| || |..||| || ||: |||  
 186 CFIQTLVDVFTKRKGHILELLTEVTRRMAEALVQEGKARKTNPEIQSTL 235  
 251 RKKLYLQ\* 257  
 ||: |||  
 236 RKRLYLQ\* 242

Fig. 10

BEST AVAILABLE COPY